

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/552,287
Source: P4710
Date Processed by STIC: 10/18/05

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER:

10/552,287

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- | | | |
|---|--|--|
| 1 | <input type="checkbox"/> Wrapped Nucleic
<input type="checkbox"/> Wrapped Aminos | The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping." |
| 2 | <input type="checkbox"/> Invalid Line Length | The rules require that a line not exceed 72 characters in length. This includes white spaces. |
| 3 | <input type="checkbox"/> Misaligned Amino
<input checked="" type="checkbox"/> Numbering | The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead. |
| 4 | <input checked="" type="checkbox"/> Non-ASCII | The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text. |
| 5 | <input type="checkbox"/> Variable Length | Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules , each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing. |
| 6 | <input type="checkbox"/> PatentIn 2.0
<input type="checkbox"/> "bug" | A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences. |
| 7 | <input type="checkbox"/> Skipped Sequences
<input type="checkbox"/> (OLD RULES) | Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped |
| Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences. | | |
| 8 | <input type="checkbox"/> Skipped Sequences
<input type="checkbox"/> (NEW RULES) | Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000 |
| 9 | <input type="checkbox"/> Use of n's or Xaa's
<input type="checkbox"/> (NEW RULES) | Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents. |
| 10 | <input type="checkbox"/> Invalid <213>
<input type="checkbox"/> Response | Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence |
| 11 | <input type="checkbox"/> Use of <220> | Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules) |
| 12 | <input type="checkbox"/> PatentIn 2.0
<input type="checkbox"/> "bug" | Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk. |
| 13 | <input type="checkbox"/> Misuse of n/Xaa | "n" can only represent a single <u>nucleotide</u> ; "Xaa" can only represent a single <u>amino acid</u> |



PCT

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/552,287

DATE: 10/18/2005
TIME: 10:13:33

Input Set : A:\PTO.RJ.txt
Output Set: N:\CRF4\10182005\J552287.raw

3 <110> APPLICANT: Futerman, Anthony
 4 Sussman, Joel
 5 Silman, Israel
 6 Harel, Michal
 7 Dvir, Hay
 8 Toker, Lilly
 9 Swetlana Adamsky
 11 <120> TITLE OF INVENTION: GAUCHER DISEASE DRUGS AND METHODS OF IDENTIFYING SAME
 13 <130> FILE REFERENCE: 30227
 C--> 15 <140> CURRENT APPLICATION NUMBER: US/10/552,287
 C--> 15 <141> CURRENT FILING DATE: 2005-10-04
 15 <160> NUMBER OF SEQ ID NOS: 16
 17 <170> SOFTWARE: PatentIn version 3.2

All item 4 on Env
 Summary
 Meet

ERRORED SEQUENCES

2007 <210> SEQ ID NO: 16
 2008 <211> LENGTH: 497
 2009 <212> TYPE: PRT
 2010 <213> ORGANISM: Pan troglodytes
 2012 <400> SEQUENCE: 16
 2014 Ala Arg Pro Cys Ile Pro Lys Ser Phe Gly Tyr Ser Ser Val Val Cys
 2015 1 5 10 15
 2018 Val Cys Asn Ala Thr Tyr Cys Asp Ser Phe Asp Pro Pro Thr Phe Pro
 2019 20 25 30
 2022 Ala Leu Gly Thr Phe Ser Arg Tyr Glu Ser Thr Arg Ser Gly Arg Arg
 2023 35 40 45
 2026 Met Glu Leu Ser Met Gly Thr Ile Gln Ala Asn His Thr Gly Thr Gly
 2027 50 55 60
 2030 Leu Leu Leu Thr Leu Gln Pro Glu Gln Lys Phe Gln Lys Val Lys Gly
 2031 65 70 75 80
 2034 Phe Gly Gly Ala Met Thr Asp Ala Ala Leu Asn Ile Leu Ala Leu
 2035 85 90 95
 2038 Ser Pro Pro Ala Gln Asn Leu Leu Lys Ser Tyr Phe Ser Glu Glu
 2039 100 105 110
 2042 Gly Ile Gly Tyr Asn Ile Ile Arg Val Pro Met Ala Ser Cys Asp Phe
 2043 115 120 125
 2046 Ser Ile Arg Thr Tyr Thr Tyr Ala Asp Thr Pro Asp Asp Phe Gln Leu
 2047 130 135 140
 2050 His Asn Phe Ser Leu Pro Glu Glu Asp Thr Lys Leu Lys Ile Pro Leu
 2051 145 150 155 160
 2054 Ile His Arg Ala Leu Gln Leu Ala Gln Arg Pro Val Ser Leu Leu Ala

Does Not Comply
 Comedical Diskette Needs

P.J.

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/552,287

DATE: 10/18/2005
TIME: 10:13:33

Input Set : A:\PTO.RJ.txt
Output Set: N:\CRF4\10182005\J552287.raw

2055	165	170	175
2058	Ser Pro Trp Thr Ser Pro Thr Trp Leu Lys Thr Asn Gly Ala Val Asn		
2059	180	185	190
2062	Gly Lys Gly Ser Leu Lys Gly Gln Pro Gly Asp Ile Tyr His Gln Thr		
2063	195	200	205
2066	Trp Ala Arg Tyr Phe Val Lys Phe Leu Asp Ala Tyr Ala Glu His Lys		
2067	210	215	220
2070	Leu Gln Phe Trp Ala Val Thr Ala Glu Asn Glu Pro Ser Ala Gly Leu		
2071	225	230	235
2074	240		
2075	Leu Ser Gly Tyr Pro Phe Gln Cys Leu Gly Phe Thr Pro Glu His Gln		
2078	245	250	255
2079	Arg Asp Phe Ile Ala Arg Asp Leu Gly Pro Thr Leu Ala Asn Ser Thr		
2082	260	265	270
2083	His His Asn Val Arg Leu Leu Met Leu Asp Asp Gln Arg Leu Leu Leu		
2086	275	280	285
2087	Pro His Trp Ala Lys Val Val Leu Thr Asp Pro Glu Ala Ala Lys Tyr		
2090	290	295	300
2091	Val His Gly Ile Ala Val His Trp Tyr Leu Asp Phe Leu Ala Pro Ala		
2094	305	310	315
2095	Lys Ala Thr Leu Gly Glu Thr His Arg Leu Phe Pro Asn Thr Met Leu		
2098	325	330	335
2099	Phe Ala Ser Glu Ala Cys Val Gly Ser Lys Phe Trp Glu Gln Ser Val		
2102	340	345	350
2103	Arg Leu Gly Ser Trp Asp Arg Gly Met Gln Tyr Ser His Ser Ile Ile		
2106	355	360	365
2107	Thr Asn Leu Leu Tyr His Val Val Gly Trp Thr Asp Trp Asn Leu Ala		
2110	370	375	380
2111	Leu Asn Pro Glu Gly Gly Pro Asn Trp Val Arg Asn Phe Val Asp Ser		
2114	385	390	395
2115	400		
2118	Pro Ile Ile Val Asp Ile Thr Lys Asp Thr Phe Tyr Lys Gln Pro Met		
2119	405	410	415
2122	Phe Tyr His Leu Gly His Phe Ser Lys Phe Ile Pro Glu Gly Ser Gln		
2123	420	425	430
2126	Arg Val Gly Leu Val Ala Ser Gln Lys Asn Asp Leu Asp Ala Val Ala		
2127	435	440	445
2130	Leu Met His Pro Asp Gly Ser Ala Val Val Val Leu Asn Arg Ser		
2131	450	455	460
2134	465	470	475
2135	Ser Lys Asp Val Pro Leu Thr Ile Lys Asp Pro Ala Val Gly Phe Leu		
2138	480		
E--> 2147	485	490	495
	Gln		

1 *delete*

see pg 3, 5-6

10/552,289

3

<210> 7
<211> 497
<212> PRT
<213> Homo sapiens

```
<220>
<221> misc_feature
<222> (496)..(496)
<223> Arg to His mutant
      -   =   ==
<400> 7
```

<400> 7

Val Cys Asn Ala Thr Tyr Cys Asp Ser Phe Asp Pro Pro Thr Phe Pro
20 25 30

Ala Leu Gly Thr Phe Ser Arg Tyr Glu Ser Thr Arg Ser Gly Arg Arg
35 40 45

Met Glu Leu Ser Met Gly Pro Ile Gln Ala Asn His Thr Gly Thr Gly
50 55 60

Leu Leu Leu Thr Leu Gln Pro Glu Gln Lys Phe Gln Lys Val Lys Gly
65 70 75 80

Ser Pro Pro Ala Gln Asn Leu Leu Leu Lys Ser Tyr Phe Ser Glu Glu
 100 105 110

Gly Ile Gly Tyr Asn Ile Ile Arg Val Pro Met Ala Ser Cys Asp Phe
115 120 125

Ser Ile Arg Thr Tyr Thr Tyr Ala Asp Thr Pro Asp Asp Asp Phe Gln Leu
130 135 140

His	Asn	Phe	Ser	Leu	Pro	Glu	Glu	Asp	Thr	Lys	Leu	Lys	Ile	Pro	Leu
145					150					155					160

Ile His Arg Ala Leu Gln Leu Ala Gln Arg Pro Val Ser Leu Leu Ala
165 170 175

10/552,287 4

Ser Pro Trp Thr Ser Pro Thr Trp Leu Lys Thr Asn Gly Ala Val Asn
180 185 190

Gly Lys Gly Ser Leu Lys Gly Gln Pro Gly Asp Ile Tyr His Gln Thr
195 200 205

Trp Ala Arg Tyr Phe Val Lys Phe Leu Asp Ala Tyr Ala Glu His Lys
210 215 220

Leu Gln Phe Trp Ala Val Thr Ala Glu Asn Glu Pro Ser Ala Gly Leu
225 230 235 240

Leu Ser Gly Tyr Pro Phe Gln Cys Leu Gly Phe Thr Pro Glu His Gln
245 250 255

Arg Asp Phe Ile Ala Arg Asp Leu Gly Pro Thr Leu Ala Asn Ser Thr
260 265 270

His His Asn Val Arg Leu Leu Met Leu Asp Asp Gln Arg Leu Leu Leu
275 280 285

Pro His Trp Ala Lys Val Val Leu Thr Asp Pro Glu Ala Ala Lys Tyr
290 295 300

Val His Gly Ile Ala Val His Trp Tyr Leu Asp Phe Leu Ala Pro Ala
305 310 315 320

Lys Ala Thr Leu Gly Glu Thr His Arg Leu Phe Pro Asn Thr Met Leu
325 330 335

Phe Ala Ser Glu Ala Cys Val Gly Ser Lys Phe Trp Glu Gln Ser Val
340 345 350

Arg Leu Gly Ser Trp Asp Arg Gly Met Gln Tyr Ser His Ser Ile Ile
355 360 365

Thr Asn Leu Leu Tyr His Val Val Gly Trp Thr Asp Trp Asn Leu Ala
370 375 380

Leu Asn Pro Glu Gly Gly Pro Asn Trp Val Arg Asn Phe Val Asp Ser
385 390 395 400

Pro Ile Ile Val Asp Ile Thr Lys Asp Thr Phe Tyr Lys Gln Pro Met

10/552,289 5

405

410

415

Phe Tyr His Leu Gly His Phe Ser Lys Phe Ile Pro Glu Gly Ser Gln
420 425 430

Arg Val Gly Leu Val Ala Ser Gln Lys Asn Asp Leu Asp Ala Val Ala
435 440 445

Leu Met Asn Pro Asp Gly Ser Ala Val Val Val Val Leu Asn Arg Ser
450 455 460

Ser Lys Asp Val Pro Leu Thr Ile Lys Asp Pro Ala Val Gly Phe Leu
465 470 475 480

Glu Thr Ile Ser Pro Gly Tyr Ser Ile His Thr Tyr Leu Trp His Arg
485 490 495

same error
in sequence 14

10/552,287 6

<210> 9
<211> 497
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> (370)..(370)
<223> Asn of Ser mutant

to

VERIFICATION SUMMARY
PATENT APPLICATION: US/10/552,287

DATE: 10/18/2005
TIME: 10:13:34

Input Set : A:\PTO.RJ.txt
Output Set: N:\CRF4\10182005\J552287.raw

L:15 M:270 C: Current Application Number differs, Replaced Current Application No
L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:2002 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:0
L:2147 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16